

PAGE MSARVRSRSGRGDQ. EAPDVVAFVAPGE. SQEEPPT
|| || | | | : : | : : ||
GAGE2 MSWRGRSTYRPRRYPVEPPMIGFMRPEQFSDEVEPAT
GAGE1 Y E M
GAGE3 K Y Q V
GAGE4 Y Q M
GAGES,6 Y Q V
|| || | : : | | : : | : : || : |
MAGES MSLEBQKSO. KPBEGLDTQE. EALGLVGVOAATTEEQEAVS
MAGES LG Y A QAG. P MD IPA KA

```

PAGE      DNQDIEPGQERE..... GTPPIERRKVEGDCQE
          :: || :: | : | ||
GAGE2     P.EEGEPATQRQDPAAAQEGEDEGASAGQGPKEAHSQE
GAGE1                                           D
GAGE3-6                                         D
          ||| | ||| | | | | | | | | | | | | | |
MAGE5     SSSPLVPGTILGEVPAAGSPGPLK.SPQGSALPTAIDFTLW
MAGE8     T IM E TDS S PO. E SSL VT S

```

```

PAGE          MDLEKTRSERGDGSUVKERTPNPKHAKTKEAGDGQP
              = | | | | : | : | | | | | : |
GAGE2         QGHPQTGCCECDGPDGQEMDPNPNPEEVKTPPEEGEKQSQC
GAGE1         M
GAGE3-5       M . MR HYVA..
GAGE6         V
              : | | : | : | | | | | : |
MAGE5         RQSIKGSSNQEEEGPSTSPDP...ESVFRAALSKKVADLIHFLLLKY
MAGE8         S DE SN AHL L E DE E VR R..

```

```
PAGE1      MSA...RVRSRSRGRGDGQEPDVVAFVAPGES.....
           ||.  |.|||.||::||::|||...|: |...|.
PAGE2      MSELVVRARSQSSSRGNDQESSQPVGSSVIVQEPTEZKR
           .....
PAGE3      .....MTSF
```

```
PAGE1      QEEPPTDNOGPD.....MEAFQOEL  
            |:||||| || :               ||||  
  
PAGE2      QQEPPTDNQDI EPGQEREGTP I ERKVEGD CQE M  
            :   ||  : || ||||| :       :    ||||  
  
PAGE3      NKTAPP IESDYTPGQERDEGALDFVPSLAATWEL
```

```
PAGE1 DLEKTRSERGDGSDVKEKT PPNPKHAXTKAEGDGQP  
      :| |: | |: || |: | |: | |: | |: |  
PAGE2 ALLKI DEPGDGP DVREGIMPTFDLTKVLEAGDAQP  
      |: | |: | |: | |: | |: | |: | |: |  
PAGE3 TRPKTGGERGDCGNVKGESLPNLSPVKIPEAGEGQPSV
```


Replacement Sheets

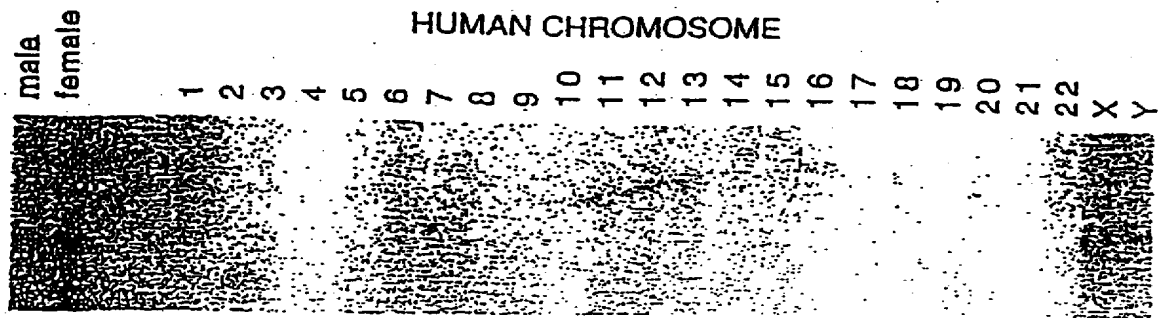


FIG. 2C

Replacement Sheets

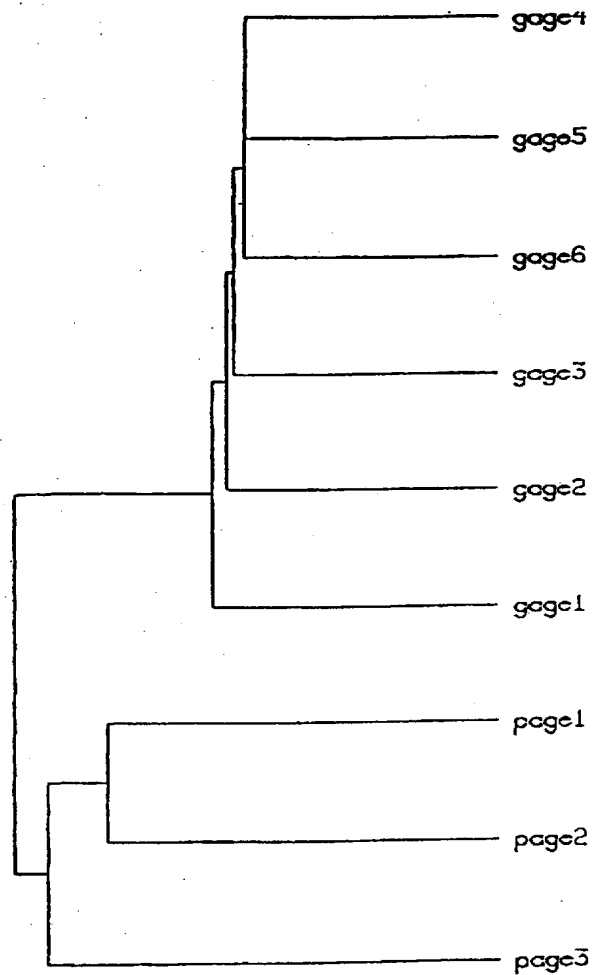


FIG. 3

Replacement Sheets

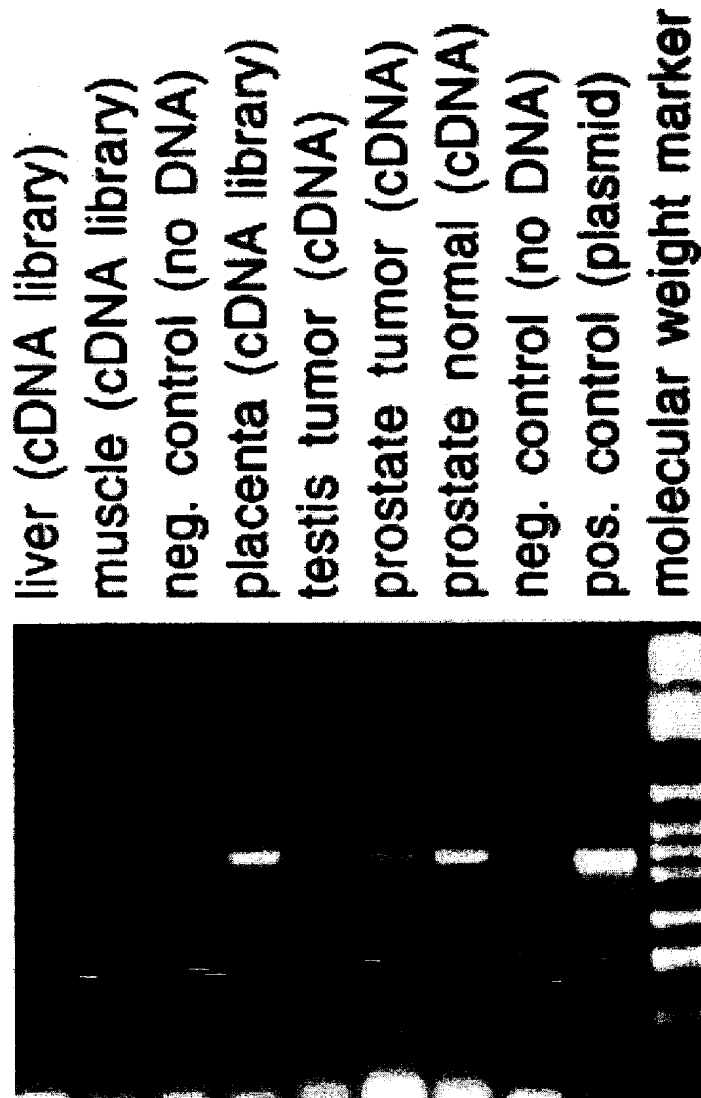


FIG. 4

Replacement Sheets

Page 4 sequence (bold and underline: open reading frame).

GAAGAATTCGCCAGGCTCTCTGCTGACTCAAGTTCTTCAGTTCACGATCTTCTAGTT
GCAGCG

ATGAGTGCACGAGTGAGATCAAGATCCAGAGGAAGAGGAGATGGTCAGGAGGCTCCC
GATGTGGTTGCATTTCGTGGCTCCCGGTGAATCTCAGCAAGAGGAACCACCAACTGAC
AATCAGGATATTGAACCTGGACAAGAGAGAGAAGGAACACCTCCGATCGAAGAACGT
AAAGTAGAAGGTGATTGCCAGGAAATGGATCTGGAAAAGACTCGGAGTGAGCGTGGA
GATGGCTCTGATGTAAAAGAGAAGACTCCACCTAATCCTAAGCATGCTAAGACTAAA
GAAGCAGGAGATGGGCAGCCA

TAAGTTAAAAAGAAGACAAGCTGAAGCTACACACATGGCTGATGTCACATT
GAAAATGTGACTGAAAATTTGAAAATTTCTCTCAATAAAGTTTGAGTTTTCTCTGAA

FIG. 5